



## SEQUENCE LISTING

## (1) GENERAL INFORMATION

(i) APPLICANT: MOORE, PAUL A.  
RUBEN, STEVEN M.  
EBNER, REINHARD

(ii) TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR-LIKE PROTEASE

(iii) NUMBER OF SEQUENCES: 16

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: HUMAN GENOME SCIENCES, INC.  
(B) STREET: 9410 KEY WEST AVENUE  
(C) CITY: ROCKVILLE  
(D) STATE: MD  
(E) COUNTRY: USA  
(F) ZIP: 20850

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/084,491  
(B) FILING DATE: 27-MAY-1998  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: BROOKES, ANDERS A.  
(B) REGISTRATION NUMBER: 36,373  
(C) REFERENCE/DOCKET NUMBER: PF378

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (301) 309-8504  
(B) TELEFAX: (301) 309-8439

## (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2329 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 124..913

(ix) FEATURE:

(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 124..184

(ix) FEATURE:

(A) NAME/KEY: mat\_peptide  
 (B) LOCATION: 187..913

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTACCAGAAC AGCATAACAA GGGCAGGTCT GACTGCAAGC TGGGACTGGG AGGCAGAGCC 60  
 GCCGCCAAGG GGGCCTCGGT TAAACACTGG TCGTTCAATC ACCTGCAAGA CGAAGAGGCA 120  
 AGG ATG CTG TTG GCC TGG GTA CAA GCA TTC CTC GTC AGC AAC ATG CTC 168  
 Met Leu Leu Ala Trp Val Gln Ala Phe Leu Val Ser Asn Met Leu  
 -21 -20 -15 -10  
 CTA GCA GAA GCC TAT GGA TCT GGA GGC TGT TTC TGG GAC AAC GGC CAC 216  
 Leu Ala Glu Ala Tyr Gly Ser Gly Gly Cys Phe Trp Asp Asn Gly His  
 -5 1 5 10  
 CTG TAC CGG GAG GAC CAG ACC TCC CCC GCG CCG GGC CTC CGC TGC CTC 264  
 Leu Tyr Arg Glu Asp Gln Thr Ser Pro Ala Pro Gly Leu Arg Cys Leu  
 15 20 25  
 AAC TGG CTG GAC GCG CAG AGC GGG CTG GCC TCG GCC CCC GTG TCG GGG 312  
 Asn Trp Leu Asp Ala Gln Ser Gly Leu Ala Ser Ala Pro Val Ser Gly  
 30 35 40  
 GCC GGC AAT CAC AGT TAC TGC CGA AAC CCG GAC GAG GAC CCG CGC GGG 360  
 Ala Gly Asn His Ser Tyr Cys Arg Asn Pro Asp Glu Asp Pro Arg Gly  
 45 50 55  
 CCC TGG TGC TAC GTC AGT GGC GAG GCC GGC GTC CCT GAG AAA CGG CCT 408  
 Pro Trp Cys Tyr Val Ser Gly Glu Ala Gly Val Pro Glu Lys Arg Pro  
 60 65 70  
 TGC GAG GAC CTG CGC TGT CCA GAG ACC ACC TCC CAG GCC CTG CCA GCC 456  
 Cys Glu Asp Leu Arg Cys Pro Glu Thr Thr Ser Gln Ala Leu Pro Ala  
 75 80 85 90  
 TTC ACG ACA GAA ATC CAG GAA GCG TCT GAA GGG CCA GGT GCA GAT GAG 504  
 Phe Thr Thr Glu Ile Gln Glu Ala Ser Glu Gly Pro Gly Ala Asp Glu  
 95 100 105  
 GTG CAG GTG TTC GCT CCT GCC AAC GCC CTG CCC GCT CGG AGT GAG GCG 552  
 Val Gln Val Phe Ala Pro Ala Asn Ala Leu Pro Ala Arg Ser Glu Ala  
 110 115 120  
 GCA GCT GTG CAG CCA GTG ATT GGG ATC AGC CAG CGG GTG CGG ATG AAC 600  
 Ala Ala Val Gln Pro Val Ile Gly Ile Ser Gln Arg Val Arg Met Asn  
 125 130 135  
 TCC AAG GAG AAA AAG GAC CTG GGA ACT CTG GGC TAC GTG CTG GGC ATT 648  
 Ser Lys Glu Lys Lys Asp Leu Gly Thr Leu Gly Tyr Val Leu Gly Ile  
 140 145 150  
 ACC ATG ATG GTG ATC ATC ATT GCC ATC GGA GCT GGC ATC ATC TTG GGC 696  
 Thr Met Met Val Ile Ile Ala Ile Gly Ala Gly Ile Ile Leu Gly  
 155 160 165 170  
 TAC TCC TAC AAG AGG GGG AAG GAT TTG AAA GAA CAG CAT GAT CAG AAA 744  
 Tyr Ser Tyr Lys Arg Gly Lys Asp Leu Lys Glu Gln His Asp Gln Lys  
 175 180 185

*0*  
*WT*

GTA TGT GAG AGG GAG ATG CAG CGA ATC ACT CTG CCC TTG TCT GCC TTC 792  
 Val Cys Glu Arg Glu Met Gln Arg Ile Thr Leu Pro Leu Ser Ala Phe  
 190 195 200

ACC AAC CCC ACC TGT GAG ATT GTG GAT GAG AAG ACT GTC GTG GTC CAC 840  
 Thr Asn Pro Thr Cys Glu Ile Val Asp Glu Lys Thr Val Val Val His  
 205 210 215

ACC AGC CAG ACT CCA GTT GAC CCT CAG GAG GGC AGC ACC CCC CTT ATG 888  
 Thr Ser Gln Thr Pro Val Asp Pro Gln Glu Gly Ser Thr Pro Leu Met  
 220 225 230

GGC CAG GCC GGG ACT CCT GGG GCC T GAGCCCCCCC AGTGGGCAGG 933  
 Gly Gln Ala Gly Thr Pro Gly Ala  
 235 240

AGCCCCATGCA GACACTGGTG CAGGACAGCC CACCCCTCCTA CAGCTAGGAG GAACTACCAC 993  
 TTTGTGTTCT GGTAAAACC CTACCACTCC CCCGCTTTT TGGCGAATCC TAGTAAGAGT 1053  
 GACAGAAGCA GGTGGCCCTG TGGGCTGAGG GTAAGGCTGG GTAGGGTCCT AACAGTGCTC 1113  
 CTTGTCCATC CCTTGGAGCA GATTTGTCT GTGGATGGAG ACAGTGGCAG CTCCCACAGT 1173  
 GATGCTGCTG CTAAGGGCTT CCAAACATTG CCTGCACCCCG TGGAAC TGAA CCAGGGATAG 1233  
 ACGGGGAGCT CCCCCAGGCT CCTCTGTGCT TTACTAAGAT GGCTCAGTCT CCACTGTGGG 1293  
 CTTGAGTGGC ATACACTGTT ATTCACTGGTT AAGGTAAAGC AGGTCAAGGG ATGGCATTGA 1353  
 AAAAAATATAT TTAGTTTTA AAATATTGG GATGGAAC TC CCTACTGACC TCTGACA ACT 1413  
 GGAAACGAGT TTGTACTGAA GTCAGAACTT TGGGTTGGGA ATGAGATCTA GGTTGTGGCT 1473  
 GCTGGTATGC TTCAGCTTGC TGGCAATGAT GTGCCTTGAC AACCGTGGGC CAGGCCTGGG 1533  
 CCCAGGGACT CTTCTGTCTT CATAAGGAAA GGAAGAATTG CACTGAGCAT TCCACTTAGG 1593  
 AAGAGGATAG AGAAGGATCT GCTCCGCCTT TGGCCACAGG AGCAGAGGCA GACCTGGGAT 1653  
 GCCCCAGTTT CTCTTCAGGG ATGGATAGTG ACCTGTCTTC ATTTGCACA GGTAAAGAGAG 1713  
 TAGTTAGCTA ACCTATGGGA ATTATACTGT GGGGCCTTGT GAGCTGCTTC TAAGAGGCTA 1773  
 ACCTGGAAAC TAAGCTCAGA GGCAAGGTAA TAAAGCACTT CAGGGCTTGC TCCCCAAGTG 1833  
 GCCCTGATTT AGCAGGTGGT CTGCGGGCGT CCAGGGTCAGC ACCTTCCTGT AGGGCACTGG 1893  
 GGCTAGGGTC ACAGCCCCTA ACTCATAAAG CAATCAAAGA ACCATTAGAA AGGGCTCATT 1953  
 AAGCCTTTG GACACAGGAC CCCAGAGAGG AAAAAGTGAC TTGCCAAGG TCGTAAGCAA 2013  
 GCTACTGGCA TGGCAAGAGC CCAGCTTCCT GACGGAGCGC AACATTTCTC CACTGCAGTG 2073  
 TGCTAGCAGC TCAGCAGGGC CTCTAACCTG TGATGTCACA CTCAAGAGGC CTTGGCAGCT 2133  
 CCTAGCCATA GAGCTTCCTT TCCAGAACCC TTCCACTGCC CAATGTGGAG ACAGGGGTTA 2193  
 GTGGGGCTTT CTATGGAGCC ATCTGCTTTG GGGACCTAGA CCTCAGGTGG TCTCTTGGTG 2253

a  
CWT

TTAGTGATGC TGGAGAAGAG AATATTACTG GTTTCTACTT TTCTATAAAG GCATTTCTCT 2313  
 ATA AAAAAAAA AAAAAA 2329

## (2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 263 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Leu Leu Ala Trp Val Gln Ala Phe Leu Val Ser Asn Met Leu Leu  
 -21 -20 -15 -10

Ala Glu Ala Tyr Gly Ser Gly Gly Cys Phe Trp Asp Asn Gly His Leu  
 -5 1 5 10

Tyr Arg Glu Asp Gln Thr Ser Pro Ala Pro Gly Leu Arg Cys Leu Asn  
 15 20 25

Trp Leu Asp Ala Gln Ser Gly Leu Ala Ser Ala Pro Val Ser Gly Ala  
 30 35 40

Gly Asn His Ser Tyr Cys Arg Asn Pro Asp Glu Asp Pro Arg Gly Pro  
 45 50 55

Trp Cys Tyr Val Ser Gly Glu Ala Gly Val Pro Glu Lys Arg Pro Cys  
 60 65 70 75

Glu Asp Leu Arg Cys Pro Glu Thr Thr Ser Gln Ala Leu Pro Ala Phe  
 80 85 90

Thr Thr Glu Ile Gln Glu Ala Ser Glu Gly Pro Gly Ala Asp Glu Val  
 95 100 105

Gln Val Phe Ala Pro Ala Asn Ala Leu Pro Ala Arg Ser Glu Ala Ala  
 110 115 120

Ala Val Gln Pro Val Ile Gly Ile Ser Gln Arg Val Arg Met Asn Ser  
 125 130 135

Lys Glu Lys Lys Asp Leu Gly Thr Leu Gly Tyr Val Leu Gly Ile Thr  
 140 145 150 155

Met Met Val Ile Ile Ala Ile Gly Ala Gly Ile Ile Leu Gly Tyr  
 160 165 170

Ser Tyr Lys Arg Gly Lys Asp Leu Lys Glu Gln His Asp Gln Lys Val  
 175 180 185

Cys Glu Arg Glu Met Gln Arg Ile Thr Leu Pro Leu Ser Ala Phe Thr  
 190 195 200

Asn Pro Thr Cys Glu Ile Val Asp Glu Lys Thr Val Val Val His Thr  
 205 210 215

*cont.*

Ser Gln Thr Pro Val Asp Pro Gln Glu Gly Ser Thr Pro Leu Met Gly  
 220 225 230 235

Gln Ala Gly Thr Pro Gly Ala  
 240

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Tyr Val Phe Lys Ala Gly Lys Tyr Ser Ser Glu Phe Cys Ser Thr Pro  
 1 5 10 15

Ala Cys Ser Glu Gly Asn Ser Asp Cys Tyr Phe Gly Asn Gly Ser Ala  
 20 25 30

Tyr Arg Gly Thr His Ser Leu Thr Glu Ser Gly Ala Ser Cys Leu Pro  
 35 40 45

Trp Asn Ser Met Ile Leu Ile Gly Lys Val Tyr Thr Ala Gln Asn Pro  
 50 55 60

Ser Ala Gln Ala Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro  
 65 70 75 80

Asp Gly Asp Ala Lys Pro Trp Cys His Val Leu Lys Asn Arg Arg Leu  
 85 90 95

Thr Trp Glu Tyr Cys Asp Val Pro Ser Cys Ser Thr Cys Gly Leu Arg  
 100 105 110

Gln Tyr Ser Gln Pro Gln Phe Arg Ile Lys Gly Gly Leu Phe Ala Asp  
 115 120 125

Ile Ala Ser His Pro Trp Gln Ala Ala Ile Phe Ala Lys His Arg Arg  
 130 135 140

Ser Pro Gly Glu Arg Phe Leu Cys Gly Gly Ile Leu Ile Ser Ser Cys  
 145 150 155 160

Trp Ile Leu Ser Ala Ala His Cys Phe Gln Glu Arg Phe Pro Pro His  
 165 170 175

His Leu Thr Val Ile Leu Gly Arg Thr Tyr Arg Val Val Pro Gly Glu  
 180 185 190

Glu Glu Gln Lys Phe Glu Val Glu Lys Tyr Ile Val His Lys Glu Phe  
 195 200 205

Asp Asp Asp Thr Tyr Asp Asn Asp Ile Ala Leu Leu Gln Leu Lys Ser

A  
 Cont.

210	215	220
Asp Ser Ser Arg Cys Ala Gln Glu Ser Ser Val Val Arg Thr Val Cys		
225	230	235
Leu Pro Pro Ala Asp Leu Gln Leu Pro Asp Trp Thr Glu Cys Glu Leu		
245	250	255
Ser Gly Tyr Gly Lys His Glu Ala Leu Ser Pro Phe Tyr Ser Glu Arg		
260	265	270
Leu Lys Glu Ala His Val Arg Leu Tyr Pro Ser Ser Arg Cys Thr Ser		
275	280	285
Gln His Leu Leu Asn Arg Thr Val Thr Asp Asn Met Leu Cys Ala Gly		
290	295	300
Asp Thr Arg Ser Gly Gly Pro Gln Ala Asn Leu His Asp Ala Cys Gln		
305	310	315
Gly Asp Ser Gly Gly Pro Leu Val Cys Leu Asn Asp Gly Arg Met Thr		
325	330	335
Leu Val Gly Ile Ile Ser Trp Gly Leu Gly Cys Gly Gln Lys Asp Val		
340	345	350
Pro Gly Val Tyr Thr Lys Val Thr Asn Tyr Leu Asp Trp Ile Arg Asp		
355	360	365
Asn Met Arg Pro		
370		

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATTGCACTGA GCATTCCACT TAGGAAGAGG ATAGAGAAGG ATCTGCTCCG CCTTTGGCCA	60
CAGGAGCAGA GGCAGACCTG GGATGCCCA TTTCTCTTCA GGGATGGATA GTGACCTGTC	120
TTCATTTGC ACAGGTAAGA GAGTAGTTAG CTAACCTATG GGAATTATAC TGTGGGCCT	180
TGTAGCTGCT TCTAAGAGGC TAACCTGGAA ACTAAGCTCA GAGGCAAGGT AATAAAGCAC	240
TTCAGGGCTT	250

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 base pairs

A  
Cont.

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATAGAGAAAT GCCTTATAG AAAAGTAGAA ACCAGTAATA TTCTCTTCTC CAGCATCACT	60
AACACCAAGA GACCACCTGA GGTCTAGGTC CCCAAAGCAG ATGGCTCCAT AGAAAGCCCC	120
ACTAACCCGT CTCCACATTG GGCAGTGGAA GGGTTCTGGA AAGGAAGCTC TATGGCTAGG	180
AGCTGCCAAG GCCTCTTGAG TGTGACATCA CAGGTTAGAG GCCCTGCTGA GCTGCTAGCA	240
CAGTGCA	247

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AATTCGGCAA GAGTAACAGC ATAACAAGGG TAGGTCTGAC TGCAGCTGGG ACTGGGAGGC	60
AGAGCACGCC AAGGGGGCCT CGGTTAAACA CTGGTCGTTA AATCACCTGC AAACGAGGAG	120
GCAAGGATGC TGTTGGCCTG GGTACAGCAT TCCTGGTCAG CAACATGCTC CTAGCGTAAG	180
CCTATGGATC TGGAGGCTGT TTCTGGGACA ACGGCCACTG TACCCGGAGG ACCAGACCTT	240
CCCGGCCGGT CCTCGTGCCT CAACTGGCTG GACGCGCAGG GCTGCCTGGG CCCCCTTTTC	300
GGTCAAATTT CACAGTTTAC TTCGAAACCG GGACGGGGCC GTGGGGGCCC TGGTGGTTAG	360
TTTGGGGTCG GGTTTCTTA AAAAAGGTTT TTGGGGCCGG TTTTCGGAAC CATTTCGGTT	420
GAATTTTTA GGGAAATTTC AGGAGTTTT TAAGGGCCAT T	461

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGCAAGTTGC AGAACTGGAA ACGAGTTGT ACAGAAGTCA GAACTTGGG TTAGGAATGA	60
GATCTAGGTT GTGGCTGCTG GTATGCTTCA TTGCTGGCAA TAATGTGCCT TGACAACCGT	120
GGGCCAGGCC TGGGACCCAGG GACTCTTCCT GTTTCATAAG GAAAGGAAGA ATTGCACGTGA	180
GCATTCCACT TAGGAAGAGG ATAGAGCAAG GAATCTGCTC CGCTTGGCC ACAGGAGCAG	240
AGGCAGACCT GGGATGCCCC AGTTCTCTT CAGGGATGGG ATAGTGACCT GTCTTACATT	300
TTGCACAGGT AAAGAGAGTT AGTTAGCTAA CCTATTGGGC TTTATTACTT GGGGCTTGTG	360
AGCTGCTTT TAAGAGGTAA ACCTGGAACT AAAGTTCA	399

## (2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TAATTCGGCA AGGGACAGGT CTGACTGCAG CTGGGACTGG GAGGCAGAGC CGTCAAGGGG	60
GCCTCGGTTA AACACTGGTC GTTCAATCAC CTGCAACGAG AGGCAAGGAT GCTGTTGGCC	120
TGGGTACAAG CATTCCGTGTC AGCAACATGC TCCTAGCAGA AAGCCTATGG ATCTGGGAGG	180
CTGTTTCTGG GACAACGGCC ACCTGTACCG GAGGACCAGA CCTCCCCGGC CGGGCCTTCC	240
GTGGCCTTCA ATTGGTTTGA CGTGGCAAAG GGGCTTGTCT GGCCCTTTG GGGGAAAATT	300
ACAAGTTTA ATTGTCCCGG AAAACCTGGA GAGG	334

## (2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 472 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AATTGGCAG AGGGAGAGGG AGATGCAGCG AATCACTCTG CCCTTGTCTG CCTTCACCAA	60
CCCCACCTGT GAGATTGTGG ATGAGAAGAC TGTGTTGGTC CACACCAGCC AGACTCCAGT	120
TGACCCTCAG GAGGGCAGCA CCCCCCTTAT GGGACCAGGC CGGGGACTCC TGGGGCCTGA	180
GCCCCCAGT GGGGCAGGAG CCATGGCAGA CACTGGTGCA GGACAGCCAC CCTCCTTACA	240
GCTAGGGGGA ACTACCACTT TGTGTTCTG GTTTAAAACC CTACCACTCC CGGATTTTT	300
GGCGGATTCC TTAGTTAAGA GTACAGAAGC AGGTGGGCCT ATGGCTTGGA GGGTAAGGTG	360
GGGTAGGGTT CCTAAAAGTG GGTTCTTGGT TGCTCCTGGG AGGAAGATT TGTTTTGGT	420
GGGGACAGTG GCAGTTCCA CAGGTTGTTG TGTTAAGGGG TTCAAAAAAT TG	472

## (2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 291 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGGCACGAGA TGAACCTCAA GGAGAAAAAG GACCTGGAA CTCTGGTAT GACGGTCCCC	60
CACCCCTGCC CTTGTTGGGA TTCATCAAGA GATGTCATT GCTGATTGTC TAGGGTGTGG	120
CTAATGGGAC CTTGTGTCCT ATCCTTGGCA GGCTACGTGC TGGCATTAC CATGATGGT	180
ATCATCATTG CCATCGGAGC TGGCATCATC TTGGGCTACT CTACAAGAGG TCAGTAGCTT	240
CTCTTCTGGG CCCTCTTAGG AGGAGGGGAG GAAGGTACAC AAAGTCAAAC T	291

## (2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGCCGACATG TCTGGAGGCT GTTTCTGG	28
--------------------------------	----

## (2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGCGGAAGCT TATTAGGCC CAGGAGTCCC GGC

33

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GGCCGGGATC CGCCATCATG CTGTTGGCCT GGGTAC

36

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GGCCGGGTAC CTTATTAGGC CCCAGGAGTC CCGGC

35

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

a  
cont.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GGCCGGGATC CGCCATCATG CTGTTGGCCT GGGTAC

36

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

*a  
cont*  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGCCGGGTAC CTTATTAGGC CCCAGGAGTC CCGGC

35

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING  
NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

**O 1 P** *E J.C.*  
MAY 24 1999  
PATENT & TRADEMARK OFFICE  
U.S. DEPARTMENT OF COMMERCE

**MAY 24 1999**  
PATENT & TRADEMARK OFFICE  
U.S. DEPARTMENT OF COMMERCE

**MAY 24 1999**  
PATENT & TRADEMARK OFFICE  
U.S. DEPARTMENT OF COMMERCE

**1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.**

**2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).**

**3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).**

**4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."**

**5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).**

**6. The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).**

**7. Other: \_\_\_\_\_**

**Applicant Must Provide:**

**An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".**

**An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.**

**A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).**

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

PatentIn Software Program Support (SIRA)

Technical Assistance.....703-287-0200

To Purchase PatentIn Software.....703-306-2600

**PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE**